

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C07H 21/04, C12P 21/06, 21/02, C12N 1/20, 15/00, C07K 1/00, 14/52	A1	(11) International Publication Number: WO 97/15586 (43) International Publication Date: 1 May 1997 (01.05.97)
(21) International Application Number: PCT/US96/16778 (22) International Filing Date: 17 October 1996 (17.10.96) (30) Priority Data: 08/553,727 23 October 1995 (23.10.95) US (71) Applicant: TULARIK, INC. [US/US]; Two Corporate Drive, South San Francisco, CA 94080 (US). (72) Inventors: BAICHWAL, Vijay, R.; Two Corporate Drive, South San Francisco, CA 94080 (US). HUANG, Jianing; Two Corporate Drive, South San Francisco, CA 94080 (US). HSU, Hailing; Two Corporate Drive, South San Francisco, CA 94080 (US). GOEDDEL, David, V.; Two Corporate Drive, South San Francisco, CA 94080 (US). (74) Agents: BREZNER, David, J. et al.; Flehr, Hohbach, Test, Albritton & Herbert, Suite 3400, 4 Embarcadero Center, San Francisco, CA 94111-4187 (US).		(81) Designated States: AU, CA, JP, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>
(54) Title: RIP: NOVEL HUMAN PROTEIN INVOLVED IN TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING ASSAYS (57) Abstract The invention relates to a human Receptor Interacting Protein (hRIP), nucleic acids which encode hRIP and methods of using the subject compositions; in particular, methods such as hRIP-based in vitro binding assays and phosphorylation assays for screening chemical libraries for lead compounds for pharmacological agents.		

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AM	Armenia	GB	United Kingdom	MW	Malawi
AT	Austria	GE	Georgia	MX	Mexico
AU	Australia	GN	Guinea	NE	Niger
BB	Barbados	GR	Greece	NL	Netherlands
BE	Belgium	HU	Hungary	NO	Norway
BF	Burkina Faso	IE	Ireland	NZ	New Zealand
BG	Bulgaria	IT	Italy	PL	Poland
BJ	Benin	JP	Japan	PT	Portugal
BR	Brazil	KE	Kenya	RO	Romania
BY	Belarus	KG	Kyrgyzstan	RU	Russian Federation
CA	Canada	KP	Democratic People's Republic of Korea	SD	Sudan
CF	Central African Republic	KR	Republic of Korea	SE	Sweden
CG	Congo	KZ	Kazakhstan	SG	Singapore
CH	Switzerland	LI	Liechtenstein	SI	Slovenia
CI	Côte d'Ivoire	LK	Sri Lanka	SK	Slovakia
CM	Cameroon	LR	Liberia	SN	Senegal
CN	China	LT	Lithuania	SZ	Swaziland
CS	Czechoslovakia	LU	Luxembourg	TD	Chad
CZ	Czech Republic	LV	Latvia	TG	Togo
DE	Germany	MC	Monaco	TJ	Tajikistan
DK	Denmark	MD	Republic of Moldova	TT	Trinidad and Tobago
EE	Estonia	MG	Madagascar	UA	Ukraine
ES	Spain	ML	Mali	UG	Uganda
FI	Finland	MN	Mongolia	US	United States of America
FR	France	MR	Mauritania	UZ	Uzbekistan
GA	Gabon			VN	Viet Nam

*RIP: Novel Human Protein Involved in Tumor Necrosis Factor
Signal Transduction, and Screening Assays*

INTRODUCTION

5 Field of the Invention

The field of this invention is a novel human kinase involved in tumor necrosis factor signal transduction and its use in drug screening.

Background

10 Tumor necrosis factor (TNF) is an important cytokine involved in the signaling of a number of cellular responses including cytotoxicity, anti-viral activity, immun.-regulatory activities and the transcriptional regulation of a number of genes. The TNF receptors (TNF-R1 and TNF-R2) are members of the larger TNF receptor superfamily which also includes the Fas antigen, CD27, CD30, CD40, and the low affinity nerve growth factor receptor. Members of this family have been shown to participate in a variety of biological properties,
15 including programmed cell death, antiviral activity and activation of the transcription factor NF- κ B in a wide variety of cell types.

Accordingly, it is desired to identify agents which specifically modulate transduction of TNF receptor family signalling. Unfortunately, the components of the signalling pathway remain largely unknown; hence, the reagents necessary for the development of high-
20 throughput screening assays for such therapeutics are unavailable. Elucidation of TNF receptor family signal transduction pathways leading to NF- κ B activation would provide valuable insight into mechanisms to alleviate inflammation. In particular, components of this pathway would provide valuable targets for automated, cost-effective, high throughput drug screening and hence would have immediate application in a broad range of domestic and
25 international pharmaceutical and biotechnology drug development programs.

Relevant Literature

Stanger et al. (1995) Cell 81, 513-523 report the existence of a Receptor Interacting Protein (RIP) and its functional expression. VanArsdale and Ware (1994) J Immunology 153:3043-3050 describe proteins associated with TNF-R1. The cloning and amino acid
30 sequencing of TNF-R1 is disclosed in Schall et al (1990) Cell 61, 361 and Loetscher et al (1990) Cell 61, 351; the identification of a "death domain" in TNF-R1 is disclosed in Tartaglia et al. (1993) Cell 74:845-853. The cloning and amino acid sequence of a TNF-R associated death domain protein (TRADD) is described by Hsu et al. (1995) Cell 81, 495-504. The cloning and amino acid sequence of the Fas antigen is disclosed in Itoh et al (1991)

Cell 66, 233-243. For a recent review, see Smith et al. (1994) Cell 76:959-962 and Vandenabelle et al. (1995) Trends Cell Biol. 5, 392-399.

SUMMARY OF THE INVENTION

5 The invention provides methods and compositions relating to a human Receptor Interacting Protein (hRIP). The compositions include nucleic acids which encode hRIP, hRIP kinase domains, and recombinant proteins made from these nucleic acids. The invention also provides methods for screening chemical libraries for lead compounds for a pharmacological agent useful in the diagnosis or treatment of disease associated hRIP activity
10 or hRIP-dependent signal transduction. In one embodiment, the methods involve incubating a mixture of hRIP, a natural intracellular hRIP substrate or binding target and a candidate pharmacological agent and determining if the presence of the agent modulates the ability of hRIP to selectively phosphorylate the substrate or bind the binding target. Specific agents provide lead compounds for pharmacological agents capable of disrupting hRIP function.

15

DETAILED DESCRIPTION OF THE INVENTION

A human RIP-encoding nucleic acid sequence is set out in SEQ ID NO: 1. A human RIP kinase domain-encoding nucleic acid sequence is set out in SEQ ID NO: 1, nucleotides 1-900. A human RIP amino acid sequence is set out in SEQ ID NO: 2; and a hRIP kinase
20 domain sequence is set out in SEQ ID NO:2, residues 1-300.

Natural nucleic acids encoding hRIP are readily isolated from cDNA libraries with PCR primers and hybridization probes containing portions of the nucleic acid sequence of SEQ ID NO:1. For example, we used low stringency hybridization at 42°C (hybridization buffer: 20% formamide, 10 % Denhardt, 0.5% SDS, 5X SSPE; with membrane washes at
25 room temperature with 5X SSPE/0.5% SDS) with a 120 base oligonucleotide probe (SEQ ID NO: 1, nucleotides 1728-1847) to isolate a native human RIP cDNA from a library prepared from human umbilical vein endothelial cells. In addition, synthetic hRIP-encoding nucleic acids may be generated by automated synthesis.

The subject nucleic acids are recombinant, meaning they comprise a sequence joined
30 to a nucleotide other than that to which sequence is naturally joined and isolated from a natural environment. The nucleic acids may be part of hRIP-expression vectors and may be incorporated into cells for expression and screening, transgenic animals for functional studies

(e.g. the efficacy of candidate drugs for disease associated with expression of a hRIP), etc. These nucleic acids find a wide variety of applications including use as templates for transcription, hybridization probes, PCR primers, therapeutic nucleic acids, etc.; use in detecting the presence of hRIP genes and gene transcripts, in detecting or amplifying nucleic acids encoding additional hRIP homologs and structural analogs, and in gene therapy applications.

The invention provides efficient methods of identifying pharmacological agents or lead compounds for agents active at the level of a hRIP modulatable cellular function, particularly hRIP mediated TNF receptor or Tumor necrosis factor receptor associated Factor -2 (TRAF2) or TRADD-induced signal transduction. For example, we have found that a binding complex comprising TNF R1, TRADD, and hRIP exists in TNF-stimulated cells. Generally, the screening methods involve assaying for compounds which interfere with a hRIP activity such as kinase activity or TRAF2 or TRADD binding. The methods are amenable to automated, cost-effective high throughput screening of chemical libraries for lead compounds. Identified reagents find use in the pharmaceutical industries for animal and human trials; for example, the reagents may be derivatized and rescreened in in vitro and in vivo assays to optimize activity and minimize toxicity for pharmaceutical development. Target therapeutic indications are limited only in that the target cellular function be subject to modulation, usually inhibition, by disruption of the formation of a complex comprising hRIP and one or more natural hRIP intracellular binding targets including substrates or otherwise modulating hRIP kinase activity. Target indications may include infection, genetic disease, cell growth and regulatory or immunologic dysfunction, such as neoplasia, inflammation, hypersensitivity, etc.

A wide variety of assays for binding agents are provided including labeled in vitro kinase assays, protein-protein binding assays, immunoassays, cell based assays, etc. The hRIP compositions used in the methods are recombinantly produced from nucleic acids having the disclosed hRIP nucleotide sequences. The hRIP may be part of a fusion product with another peptide or polypeptide, e.g. a polypeptide that is capable of providing or enhancing protein-protein binding, stability under assay conditions (e.g. a tag for detection or anchoring), etc.

The assay mixtures comprise one or more natural intracellular hRIP binding targets including substrates, such as TRADD, TRAF2, or, in the case of an autophosphorylation

assay, the hRIP itself can function as the binding target. In one embodiment, the mixture comprises a complex of hRIP, TRADD and TNFR1. A hRIP derived pseudosubstrate may be used or modified (e.g. A to S/T substitutions) to generate effective substrates for use in the subject kinase assays as can synthetic peptides or other protein substrates. Generally, hRIP-
5 specificity of the binding agent is shown by kinase activity (i.e. the agent demonstrates activity of an hRIP substrate, agonist, antagonist, etc.) or binding equilibrium constants (usually at least about 10^6 M^{-1} , preferably at least about 10^8 M^{-1} , more preferably at least about 10^9 M^{-1}). A wide variety of cell-based and cell-free assays may be used to demonstrate hRIP-specific binding; preferred are rapid in vitro, cell-free assays such as mediating or
10 inhibiting hRIP-protein (e.g. hRIP-TRADD) binding, phosphorylation assays, immunoassays, etc.

The assay mixture also comprises a candidate pharmacological agent. Candidate agents encompass numerous chemical classes, though typically they are organic compounds; preferably small organic compounds and are obtained from a wide variety of sources
15 including libraries of synthetic or natural compounds. A variety of other reagents may also be included in the mixture. These include reagents like salts, buffers, neutral proteins, e.g. albumin, detergents, etc. which may be used to facilitate optimal binding and/or reduce non-specific or background interactions, etc. Also, reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, antimicrobial agents, etc. may
20 be used.

In a preferred in vitro, binding assay, a mixture of at least the kinase domain of hRIP, one or more binding targets or substrates and the candidate agent is incubated under conditions whereby, but for the presence of the candidate pharmacological agent, the hRIP specifically binds the cellular binding target at a first binding affinity or phosphorylates the
25 substrate at a first rate. After incubation, a second binding affinity or rate is detected. Detection may be effected in any convenient way. For cell-free binding assays, one of the components usually comprises or is coupled to a label. The label may provide for direct detection as radioactivity, luminescence, optical or electron density, etc. or indirect detection such as an epitope tag, an enzyme, etc. A variety of methods may be used to detect the label
30 depending on the nature of the label and other assay components. For example, the label may be detected bound to the solid substrate or a portion of the bound complex containing the label may be separated from the solid substrate, and thereafter the label detected.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLES

- 5 1. Protocol for hRIP autophosphorylation assay.
- A. Reagents:
- Neutralite Avidin: 20 µg/ml in PBS.
- hRIP: 10^{-8} - 10^{-5} M biotinylated hRIP kinase domain, residues 1-300 at 20 µg/ml in
10 PBS.
- Blocking buffer: 5% BSA, 0.5% Tween 20 in PBS; 1 hour at room temperature.
- Assay Buffer: 100 mM KCl, 20 mM HEPES pH 7.6, 0.25 mM EDTA, 1% glycerol,
 0.5% NP-40, 50 mM BME, 1 mg/ml BSA, cocktail of protease inhibitors.
- [32 P]γ-ATP 10x stock: 2×10^{-5} M cold ATP with 100 µCi [32 P]γ-ATP. Place in the
 4°C microfridge during screening.
- 15 - Protease inhibitor cocktail (1000X): 10 mg Trypsin Inhibitor (BMB # 109894), 10
 mg Aprotinin (BMB # 236624), 25 mg Benzamidine (Sigma # B-6506), 25 mg Leupeptin
 (BMB # 1017128), 10 mg APMSF (BMB # 917575), and 2mM NaVO₃ (Sigma # S-6508) in
 10 ml PBS.
- B. Preparation of assay plates:
- 20 - Coat with 120 µl of stock Neutralite avidin per well overnight at 4°C.
- Wash 2 times with 200 µl PBS.
- Block with 150 µl of blocking buffer.
- Wash 2 times with 200 µl PBS.
- C. Assay:
- 25 - Add 40 µl assay buffer/well.
- Add 40 µl biotinylated hRIP (0.1-10 pmoles/40 ul in assay buffer)
- Add 10 µl compound or extract.
- Add 10 µl [32 P]γ-ATP 10x stock.
- Shake at 30°C for 15 minutes.
- 30 - Incubate additional 45 minutes at 30°C.
- Stop the reaction by washing 4 times with 200 µl PBS.
- Add 150 µl scintillation cocktail.

- Count in Topcount.

D. Controls for all assays (located on each plate):

- a. Non-specific binding (no RIP added)
- b. cold ATP to achieve 80% inhibition.

5

2. Protocol for hRIP - substrate phosphorylation assay.

A. Reagents:

- Neutralite Avidin: 20 µg/ml in PBS.

- hRIP: 10^{-8} - 10^{-5} M hRIP at 20 µg/ml in PBS.

10 - Blocking buffer: 5% BSA, 0.5% Tween 20 in PBS; 1 hour at room temperature.

- Assay Buffer: 100 mM KCl, 20 mM HEPES pH 7.6, 0.25 mM EDTA, 1% glycerol, 0.5% NP-40, 50 mM BME, 1 mg/ml BSA, cocktail of protease inhibitors.

- [32 P]γ-ATP 10x stock: 2×10^{-5} M cold ATP with 100 µCi [32 P]γ-ATP. Place in the 4°C microfridge during screening.

15 - Substrate: 2×10^{-6} M biotinylated synthetic peptide kinase substrate at 20 µg/ml in PBS.

- Protease inhibitor cocktail (1000X): 10 mg Trypsin Inhibitor (BMB # 109894), 10 mg Aprotinin (BMB # 236624), 25 mg Benzamidine (Sigma # B-6506), 25 mg Leupeptin (BMB # 1017128), 10 mg APMSF (BMB # 917575), and 2mM NaVo₃ (Sigma # S-6508) in 10 ml PBS.

20

B. Preparation of assay plates:

- Coat with 120 µl of stock Neutralite avidin per well overnight at 4°C.

- Wash 2 times with 200 µl PBS.

- Block with 150 µl of blocking buffer.

25 - Wash 2 times with 200 µl PBS.

C. Assay:

- Add 40 µl assay buffer/well.

- Add 40 µl hRIP (0.1-10 pmoles/40 ul in assay buffer)

- Add 10 µl compound or extract.

30 - Shake at 30°C for 15 minutes.

- Add 10 µl [32 P]γ-ATP 10x stock.

- Add 10 µl substrate.

- Shake at 30°C for 15 minutes.
- Incubate additional 45 minutes at 30°C.
- Stop the reaction by washing 4 times with 200 µl PBS.
- Add 150 µl scintillation cocktail.
- 5 - Count in Topcount.
- D. Controls for all assays (located on each plate):
 - a. Non-specific binding (no RIP added)
 - b. cold ATP to achieve 80% inhibition.
- 10 3. Protocol for hRIP - TRADD binding assay.
- A. Reagents:
 - Anti-myc antibody: 20 µg/ml in PBS.
 - Blocking buffer: 5% BSA, 0.5% Tween 20 in PBS; 1 hour at room temperature.
 - Assay Buffer: 100 mM KCl, 20 mM HEPES pH 7.6, 0.25 mM EDTA, 1% glycerol,
 - 15 0.5% NP-40, 50 mM β-mercaptoethanol, 1 mg/ml BSA, cocktail of protease inhibitors.
 - ³²P hRIP 10x stock: 10^{-8} - 10^{-6} M "cold" hRIP (full length) supplemented with 200,000-250,000 cpm of labeled hRIP (HMK-tagged) (Beckman counter). Place in the 4°C microfridge during screening.
 - Protease inhibitor cocktail (1000X): 10 mg Trypsin Inhibitor (BMB # 109894), 10
 - 20 mg Aprotinin (BMB # 236624), 25 mg Benzamidine (Sigma # B-6506), 25 mg Leupeptin (BMB # 1017128), 10 mg APMSF (BMB # 917575), and 2mM NaVO₃ (Sigma # S-6508) in 10 ml PBS.
 - TRADD: 10^{-8} - 10^{-5} M myc epitope-tagged TRADD in PBS.
 - B. Preparation of assay plates:
 - 25 - Coat with 120 µl of stock anti-myc antibody per well overnight at 4°C.
 - Wash 2X with 200 µl PBS.
 - Block with 150 µl of blocking buffer.
 - Wash 2X with 200 µl PBS.
 - C. Assay:
 - 30 - Add 40 µl assay buffer/well.
 - Add 10 µl compound or extract.
 - Add 10 µl ³²P-RIP (20,000-25,000 cpm/0.1-10 pmoles/well = 10^{-9} - 10^{-7} M final

concentration).

- Shake at 25°C for 15 minutes.
- Incubate additional 45 minutes at 25°C.
- Add 40 µl eptitope-tagged TRADD (0.1-10 pmoles/40 ul in assay buffer)
- 5 - Incubate 1 hour at room temperature.
- Stop the reaction by washing 4 times with 200 µl PBS.
- Add 150 µl scintillation cocktail.
- Count in Topcount.

D. Controls for all assays (located on each plate):

- 10 a. Non-specific binding (no hRIP added)
- b. Soluble (non-tagged TRADD) to achieve 80% inhibition.

4. Protocol for hRIP - TRAF2 binding assay.

A. Reagents:

- 15 - Anti-myc antibody: 20 µg/ml in PBS.
- Blocking buffer: 5% BSA, 0.5% Tween 20 in PBS; 1 hour at room temperature.
- Assay Buffer: 100 mM KCl, 20 mM HEPES pH 7.6, 0.25 mM EDTA, 1% glycerol, 0.5% NP-40, 50 mM β-mercaptoethanol, 1 mg/ml BSA, cocktail of protease inhibitors.
- ³²P hRIP 10x stock: 10⁻⁸ - 10⁻⁶ M "cold" hRIP kinase domain, residues 1-300,
- 20 supplemented with 200,000-250,000 cpm of labeled hRIP kinase domain (HMK-tagged) (Beckman counter). Place in the 4°C microfridge during screening.
- Protease inhibitor cocktail (1000X): 10 mg Trypsin Inhibitor (BMB # 109894), 10 mg Aprotinin (BMB # 236624), 25 mg Benzamidine (Sigma # B-6506), 25 mg Leupeptin (BMB # 1017128), 10 mg APMSF (BMB # 917575), and 2mM NaVo₃ (Sigma # S-6508) in
- 25 10 ml PBS.

- TRAF2: 10⁻⁸ - 10⁻⁵ M myc eptitope-tagged TRAF2 in PBS.

B. Preparation of assay plates:

- Coat with 120 µl of stock anti-myc antibody per well overnight at 4°C.
- Wash 2X with 200 µl PBS.
- 30 - Block with 150 µl of blocking buffer.
- Wash 2X with 200 µl PBS.

C. Assay:

- Add 40 µl assay buffer/well.
- Add 10 µl compound or extract.
- Add 10 µl ³³P-RIP kinase domain (20,000-25,000 cpm/0.1-10 pmoles/well = 10^{-9} - 10^{-7} M final concentration).

5

- Shake at 25°C for 15 minutes.
- Incubate additional 45 minutes at 25°C.
- Add 40 µl epitope-tagged TRAF2 (0.1-10 pmoles/40 ul in assay buffer)
- Incubate 1 hour at room temperature.
- Stop the reaction by washing 4 times with 200 µl PBS.

10

- Add 150 µl scintillation cocktail.
- Count in Topcount.

D. Controls for all assays (located on each plate):

- a. Non-specific binding (no hRIP kinase domain added)
- b. Soluble (non-tagged TRAF2) to achieve 80% inhibition.

15

20

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: BAICHWAL, VIJAY R
HUANG, JIANING
HSU, HAILING
GOEDEL, DAVID V

(ii) TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN
TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING
ASSAYS

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
(B) STREET: 4 EMBARCADERO CENTER, SUITE 3400
(C) CITY: SAN FRANCISCO
(D) STATE: CALIFORNIA
(E) COUNTRY: USA
(F) ZIP: 94111-4187

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: BREZNER, DAVID J
(B) REGISTRATION NUMBER: 24,774
(C) REFERENCE/DOCKET NUMBER: T95-006/PCT

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 781-1989
(B) TELEFAX: (415) 398-3249

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2016 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..2013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	ATG CAA CCA GAC ATG TCC TTG AAT GTC ATT AAG ATG AAA TCC AGT GAC	48
	Met Gln Pro Asp Met Ser Leu Asn Val Ile Lys Met Lys Ser Ser Asp	
	1 5 10 15	
5	TTC CTG GAG AGT GCA GAA CTG GAC AGC GGA GGC TTT GGG AAG GTG TCT	96
	Phe Leu Glu Ser Ala Glu Leu Asp Ser Gly Gly Phe Gly Lys Val Ser	
	20 25 30	
	CTG TGT TTC CAC AGA ACC CAG GGA CTC ATG ATC ATG AAA ACA GTG TAC	144
	Leu Cys Phe His Arg Thr Gln Gly Leu Met Ile Met Lys Thr Val Tyr	
	35 40 45	
10	AAG GGG CCC AAC TGC ATT GAG CAC AAC GAG GCC CTC TTG GAG GAG GCG	192
	Lys Gly Pro Asn Cys Ile Glu His Asn Glu Ala Leu Leu Glu Glu Ala	
	50 55 60	
	AAG ATG ATG AAC AGA CTG AGA CAC AGC CGG GTG GTG AAG CTC CTG GGC	240
	Lys Met Met Asn Arg Leu Arg His Ser Arg Val Val Lys Leu Leu Gly	
15	65 70 75 80	
	GTC ATC ATA GAG GAA GGG AAG TAC TCC CTG GTG ATG GAG TAC ATG GAG	288
	Val Ile Ile Glu Glu Gly Lys Tyr Ser Leu Val Met Glu Tyr Met Glu	
	85 90 95	
20	AAG GGC AAC CTG ATG CAC GTG CTG AAA GCC GAG ATG AGT ACT CCG CTT	336
	Lys Gly Asn Leu Met His Val Leu Lys Ala Glu Met Ser Thr Pro Leu	
	100 105 110	
	TCT GTA AAA GGA AGG ATA ATT TGG GAA ATC ATT GAA GGA ATG TGC TAC	384
	Ser Val Lys Gly Arg Ile Ile Trp Glu Ile Ile Glu Gly Met Cys Tyr	
	115 120 125	
25	TTA CAT GGA AAA GGC GTG ATA CAC AAG GAC CTG AAG CCT GAA AAT ATC	432
	Leu His Gly Lys Gly Val Ile His Lys Asp Leu Lys Pro Glu Asn Ile	
	130 135 140	
	CTT GTT GAT AAT GAC TTC CAC ATT AAG ATC GCA GAC CTC GGC CTT GCC	480
	Leu Val Asp Asn Asp Phe His Ile Lys Ile Ala Asp Leu Gly Leu Ala	
30	145 150 155 160	
	TCC TTT AAG ATG TGG AGC AAA CTG AAT AAT GAA GAG CAC AAT GAG CTG	528
	Ser Phe Lys Met Trp Ser Lys Leu Asn Asn Glu Glu His Asn Glu Leu	
	165 170 175	
35	AGG GAA GTG GAC GGC ACC GCT AAG AAG AAT GGC GGC ACC CTC TAC TAC	576
	Arg Glu Val Asp Gly Thr Ala Lys Lys Asn Gly Gly Thr Leu Tyr Tyr	
	180 185 190	
	ATG GCG CCC GAG CAC CTG AAT GAC GTC AAC GCA AAG CCC ACA GAG AAG	624
	Met Ala Pro Glu His Leu Asn Asp Val Asn Ala Lys Pro Thr Glu Lys	
	195 200 205	
40	TCG GAT GTG TAC AGC TTT GCT GTA GTA CTC TGG GCG ATA TTT GCA AAT	672
	Ser Asp Val Tyr Ser Phe Ala Val Val Leu Trp Ala Ile Phe Ala Asn	
	210 215 220	
	AAG GAG CCA TAT GAA AAT GCT ATC TGT GAG CAG CAG TTG ATA ATG TGC	720
	Lys Glu Pro Tyr Glu Asn Ala Ile Cys Glu Gln Gln Leu Ile Met Cys	
45	225 230 235 240	

	ATA AAA TCT GGG AAC AGG CCA GAT GTG GAT GAC ATC ACT GAG TAC TGC	768
	Ile Lys Ser Gly Asn Arg Pro Asp Val Asp Asp Ile Thr Glu Tyr Cys	
	245 250 255	
5	CCA AGA GAA ATT ATC AGT CTC ATG AAG CTC TGC TGG GAA GCG AAT CCG	816
	Pro Arg Glu Ile Ile Ser Leu Met Lys Leu Cys Trp Glu Ala Asn Pro	
	260 265 270	
	GAA GCT CGG CCG ACA TTT CCT GGC ATT GAA GAA AAA TTT AGG CCT TTT	864
	Glu Ala Arg Pro Thr Phe Pro Gly Ile Glu Glu Lys Phe Arg Pro Phe	
	275 280 285	
10	TAT TTA AGT CAA TTA GAA GAA AGT GTA GAA GAG GAC GTG AAG AGT TTA	912
	Tyr Leu Ser Gln Leu Glu Glu Ser Val Glu Glu Asp Val Lys Ser Leu	
	290 295 300	
	AAG AAA GAG TAT TCA AAC GAA AAT GCA GTT GTG AAG AGA ATG CAG TCT	960
	Lys Lys Glu Tyr Ser Asn Glu Asn Ala Val Val Lys Arg Met Gln Ser	
15	305 310 315 320	
	CTT CAA CTT GAT TGT GTG GCA GTA CCT TCA AGC CGG TCA AAT TCA GCC	1008
	Leu Gln Leu Asp Cys Val Ala Val Pro Ser Ser Arg Ser Asn Ser Ala	
	325 330 335	
	ACA GAA CAG CCT GGT TCA CTG CAC AGT TCC CAG GGA CTT GGG ATG GGT	1056
20	Thr Glu Gln Pro Gly Ser Leu His Ser Ser Gln Gly Leu Gly Met Gly	
	340 345 350	
	CCT GTG GAG GAG TCC TGG TTT GCT CCT TCC CTG GAG CAC CCA CAA GAA	1104
	Pro Val Glu Glu Ser Trp Phe Ala Pro Ser Leu Glu His Pro Gln Glu	
	355 360 365	
25	GAG AAT GAG CCC AGC CTG CAG AGT AAA CTC CAA GAC GAA GCC AAC TAC	1152
	Glu Asn Glu Pro Ser Leu Gln Ser Lys Leu Gln Asp Glu Ala Asn Tyr	
	370 375 380	
	CAT CTT TAT GGC AGC CGC ATG GAC AGG CAG ACG AAA CAG CAG CCC AGA	1200
	His Leu Tyr Gly Ser Arg Met Asp Arg Gln Thr Lys Gln Gln Pro Arg	
30	385 390 395 400	
	CAG AAT GTG GCT TAC AAC AGA GAG GAG GAA AGG AGA CGC AGG GTC TCC	1248
	Gln Asn Val Ala Tyr Asn Arg Glu Glu Glu Arg Arg Arg Arg Val Ser	
	405 410 415	
	CAT GAC CCT TTT GCA CAG CAA AGA CCT TAC GAG AAT TTT CAG AAT ACA	1296
35	His Asp Pro Phe Ala Gln Gln Arg Pro Tyr Glu Asn Phe Gln Asn Thr	
	420 425 430	
	GAG GGA AAA GGC ACT GTT TAT TCC AGT GCA GCC AGT CAT GGT AAT GCA	1344
	Glu Gly Lys Gly Thr Val Tyr Ser Ser Ala Ala Ser His Gly Asn Ala	
	435 440 445	
40	GTG CAC CAG CCC TCA GGG CTC ACC AGC CAA CCT CAA GTA CTG TAT CAG	1392
	Val His Gln Pro Ser Gly Leu Thr Ser Gln Pro Gln Val Leu Tyr Gln	
	450 455 460	
	AAC AAT GGA TTA TAT AGC TCA CAT GGC TTT GGA ACA AGA CCA CTG GAT	1440
	Asn Asn Gly Leu Tyr Ser Ser His Gly Phe Gly Thr Arg Pro Leu Asp	
45	465 470 475 480	

	CCA GGA ACA GCA GGT CCC AGA GTT TGG TAC AGG CCA ATT CCA AGT CAT	1488
	Pro Gly Thr Ala Gly Pro Arg Val Trp Tyr Arg Pro Ile Pro Ser His	
	485 490 495	
5	ATG CCT AGT CTG CAT AAT ATC CCA GTG CCT GAG ACC AAC TAT CTA GGA	1536
	Met Pro Ser Leu His Asn Ile Pro Val Pro Glu Thr Asn Tyr Leu Gly	
	500 505 510	
	AAT ACA CCC ACC ATG CCA TTC AGC TCC TTG CCA CCA ACA GAT GAA TCT	1584
	Asn Thr Pro Thr Met Pro Phe Ser Ser Leu Pro Pro Thr Asp Glu Ser	
	515 520 525	
10	ATA AAA TAT ACC ATA TAC AAT AGT ACT GGC ATT CAG ATT GGA GCC TAC	1632
	Ile Lys Tyr Thr Ile Tyr Asn Ser Thr Gly Ile Gln Ile Gly Ala Tyr	
	530 535 540	
	AAT TAT ATG GAG ATT GGT GGG ACG AGT TCA TCA CTA CTA GAC AGC ACA	1680
	Asn Tyr Met Glu Ile Gly Gly Thr Ser Ser Ser Leu Leu Asp Ser Thr	
15	545 550 555 560	
	AAT ACG AAC TTC AAA GAA GAG CCA GCT GCT AAG TAC CAA GCT ATC TTT	1728
	Asn Thr Asn Phe Lys Glu Glu Pro Ala Ala Lys Tyr Gln Ala Ile Phe	
	565 570 575	
	GAT AAT ACC ACT AGT CTG ACG GAT AAA CAC CTG GAC CCA ATC AGG GAA	1776
20	Asp Asn Thr Thr Ser Leu Thr Asp Lys His Leu Asp Pro Ile Arg Glu	
	580 585 590	
	AAT CTG GGA AAG CAC TGG AAA AAC TGT GCC CGT AAA CTG GGC TTC ACA	1824
	Asn Leu Gly Lys His Trp Lys Asn Cys Ala Arg Lys Leu Gly Phe Thr	
	595 600 605	
25	CAG TCT CAG ATT GAT GAA ATT GAC CAT GAC TAT GAG CGA GAT GGA CTG	1872
	Gln Ser Gln Ile Asp Glu Ile Asp His Asp Tyr Glu Arg Asp Gly Leu	
	610 615 620	
	AAA GAA AAG GTT TAC CAG ATG CTC CAA AAG TGG GTG ATG AGG GAA GGC	1920
	Lys Glu Lys Val Tyr Gln Met Leu Gln Lys Trp Val Met Arg Glu Gly	
30	625 630 635 640	
	ATA AAG GGA GCC ACG GTG GGG AAG CTG GCC CAG GCG CTC CAC CAG TGT	1968
	Ile Lys Gly Ala Thr Val Gly Lys Leu Ala Gln Ala Leu His Gln Cys	
	645 650 655	
	TCC AGG ATC GAC CTT CTG AGC AGC TTG ATT TAC GTC AGC CAG AAC	2013
35	Ser Arg Ile Asp Leu Leu Ser Ser Leu Ile Tyr Val Ser Gln Asn	
	660 665 670	
	TAA	2016

(2) INFORMATION FOR SEQ ID NO:2:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 671 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Met	Gln	Pro	Asp	Met	Ser	Leu	Asn	Val	Ile	Lys	Met	Lys	Ser	Ser	Asp
	1				5					10					15	
	Phe	Leu	Glu	Ser	Ala	Glu	Leu	Asp	Ser	Gly	Gly	Phe	Gly	Lys	Val	Ser
				20					25					30		
5	Leu	Cys	Phe	His	Arg	Thr	Gln	Gly	Leu	Met	Ile	Met	Lys	Thr	Val	Tyr
			35					40					45			
	Lys	Gly	Pro	Asn	Cys	Ile	Glu	His	Asn	Glu	Ala	Leu	Leu	Glu	Glu	Ala
		50					55					60				
	Lys	Met	Met	Asn	Arg	Leu	Arg	His	Ser	Arg	Val	Val	Lys	Leu	Leu	Gly
10		65				70				75					80	
	Val	Ile	Ile	Glu	Glu	Gly	Lys	Tyr	Ser	Leu	Val	Met	Glu	Tyr	Met	Glu
				85					90					95		
	Lys	Gly	Asn	Leu	Met	His	Val	Leu	Lys	Ala	Glu	Met	Ser	Thr	Pro	Leu
				100					105					110		
15	Ser	Val	Lys	Gly	Arg	Ile	Ile	Trp	Glu	Ile	Ile	Glu	Gly	Met	Cys	Tyr
			115					120					125			
	Leu	His	Gly	Lys	Gly	Val	Ile	His	Lys	Asp	Leu	Lys	Pro	Glu	Asn	Ile
		130					135					140				
	Leu	Val	Asp	Asn	Asp	Phe	His	Ile	Lys	Ile	Ala	Asp	Leu	Gly	Leu	Ala
20		145				150					155				160	
	Ser	Phe	Lys	Met	Trp	Ser	Lys	Leu	Asn	Asn	Glu	Glu	His	Asn	Glu	Leu
				165					170					175		
	Arg	Glu	Val	Asp	Gly	Thr	Ala	Lys	Lys	Asn	Gly	Gly	Thr	Leu	Tyr	Tyr
			180						185					190		
25	Met	Ala	Pro	Glu	His	Leu	Asn	Asp	Val	Asn	Ala	Lys	Pro	Thr	Glu	Lys
			195					200					205			
	Ser	Asp	Val	Tyr	Ser	Phe	Ala	Val	Val	Leu	Trp	Ala	Ile	Phe	Ala	Asn
		210				215						220				
	Lys	Glu	Pro	Tyr	Glu	Asn	Ala	Ile	Cys	Glu	Gln	Gln	Leu	Ile	Met	Cys
30		225				230					235				240	
	Ile	Lys	Ser	Gly	Asn	Arg	Pro	Asp	Val	Asp	Asp	Ile	Thr	Glu	Tyr	Cys
				245						250				255		
	Pro	Arg	Glu	Ile	Ile	Ser	Leu	Met	Lys	Leu	Cys	Trp	Glu	Ala	Asn	Pro
			260						265					270		
35	Glu	Ala	Arg	Pro	Thr	Phe	Pro	Gly	Ile	Glu	Glu	Lys	Phe	Arg	Pro	Phe
			275					280					285			
	Tyr	Leu	Ser	Gln	Leu	Glu	Glu	Ser	Val	Glu	Glu	Asp	Val	Lys	Ser	Leu
		290				295						300				
	Lys	Lys	Glu	Tyr	Ser	Asn	Glu	Asn	Ala	Val	Val	Lys	Arg	Met	Gln	Ser
40		305				310					315				320	
	Leu	Gln	Leu	Asp	Cys	Val	Ala	Val	Pro	Ser	Ser	Arg	Ser	Asn	Ser	Ala
				325						330				335		
	Thr	Glu	Gln	Pro	Gly	Ser	Leu	His	Ser	Ser	Gln	Gly	Leu	Gly	Met	Gly
			340						345				350			
45																

Pro Val Glu Glu Ser Trp Phe Ala Pro Ser Leu Glu His Pro Gln Glu
 355 360 365
 Glu Asn Glu Pro Ser Leu Gln Ser Lys Leu Gln Asp Glu Ala Asn Tyr
 370 375 380
 5 His Leu Tyr Gly Ser Arg Met Asp Arg Gln Thr Lys Gln Gln Pro Arg
 385 390 395 400
 Gln Asn Val Ala Tyr Asn Arg Glu Glu Glu Arg Arg Arg Arg Val Ser
 405 410 415
 His Asp Pro Phe Ala Gln Gln Arg Pro Tyr Glu Asn Phe Gln Asn Thr
 10 420 425 430
 Glu Gly Lys Gly Thr Val Tyr Ser Ser Ala Ala Ser His Gly Asn Ala
 435 440 445
 Val His Gln Pro Ser Gly Leu Thr Ser Gln Pro Gln Val Leu Tyr Gln
 450 455 460
 15 Asn Asn Gly Leu Tyr Ser Ser His Gly Phe Gly Thr Arg Pro Leu Asp
 465 470 475 480
 Pro Gly Thr Ala Gly Pro Arg Val Trp Tyr Arg Pro Ile Pro Ser His
 485 490 495
 Met Pro Ser Leu His Asn Ile Pro Val Pro Glu Thr Asn Tyr Leu Gly
 20 500 505 510
 Asn Thr Pro Thr Met Pro Phe Ser Ser Leu Pro Pro Thr Asp Glu Ser
 515 520 525
 Ile Lys Tyr Thr Ile Tyr Asn Ser Thr Gly Ile Gln Ile Gly Ala Tyr
 530 535 540
 25 Asn Tyr Met Glu Ile Gly Gly Thr Ser Ser Ser Leu Leu Asp Ser Thr
 545 550 555 560
 Asn Thr Asn Phe Lys Glu Glu Pro Ala Ala Lys Tyr Gln Ala Ile Phe
 565 570 575
 Asp Asn Thr Thr Ser Leu Thr Asp Lys His Leu Asp Pro Ile Arg Glu
 30 580 585 590
 Asn Leu Gly Lys His Trp Lys Asn Cys Ala Arg Lys Leu Gly Phe Thr
 595 600 605
 Gln Ser Gln Ile Asp Glu Ile Asp His Asp Tyr Glu Arg Asp Gly Leu
 610 615 620
 35 Lys Glu Lys Val Tyr Gln Met Leu Gln Lys Trp Val Met Arg Glu Gly
 625 630 635 640
 Ile Lys Gly Ala Thr Val Gly Lys Leu Ala Gln Ala Leu His Gln Cys
 645 650 655
 Ser Arg Ile Asp Leu Leu Ser Ser Leu Ile Tyr Val Ser Gln Asn
 40 660 665 670

WHAT IS CLAIMED IS:

1. An isolated, recombinant nucleic acid encoding a human Receptor Interacting Protein (hRIP) kinase domain.
- 5 2. An isolated, recombinant nucleic acid encoding a human Receptor Interacting Protein (hRIP) comprising SEQ ID NO: 1.
3. A method of making a human Receptor Interacting Protein (hRIP) kinase domain containing protein, said method comprising the steps of translating a nucleic acid according to claim 1 to form a translation product and isolating said translation product.
- 10 4. A method of identifying lead compounds for a pharmacological agent useful in the diagnosis or treatment of disease, said method comprising the steps of:
making a protein according to the method of claim 3,
15 forming a mixture comprising:
said protein,
a natural intracellular hRIP binding target, wherein said binding target is capable of specifically binding said protein, and
a candidate pharmacological agent;
20 incubating said mixture under conditions whereby, but for the presence of said candidate pharmacological agent, said protein selectively binds said binding target at a first binding affinity;
detecting a second binding affinity of said protein to said binding target,
wherein a difference between said first and second binding affinity indicates that said
25 candidate pharmacological agent is a lead compound for a pharmacological agent capable of modulating hRIP-dependent signal transduction.
5. A method according to claim 4, wherein said hRIP binding target comprises a Tumor necrosis factor receptor Associated Factor -2 (TRAF2) or a Tumor necrosis factor Receptor-1 Associated Death Domain protein (TRADD).
- 30

6. A method of identifying lead compounds for a pharmacological agent useful in the diagnosis or treatment of disease, said method comprising the steps of:
- making a protein according to the method of claim 3,
 - forming a mixture comprising:
 - 5 said protein,
 - an hRIP substrate, wherein said hRIP kinase domain of said protein is capable of specifically phosphorylating said substrate, and
 - a candidate pharmacological agent;
 - incubating said mixture under conditions whereby, but for the presence of said
 - 10 candidate pharmacological agent, said hRIP kinase domain selectively phosphorylates said substrate at a first rate;
 - detecting a second rate of phosphorylation of said substrate by said hRIP kinase domain,
 - wherein a difference between said first and second rate indicates that said candidate
 - 15 pharmacological agent is a lead compound for a pharmacological agent capable of modulating hRIP kinase activity.
7. A method according to claim 6 wherein said hRIP substrate is hRIP.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/16778

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : Please See Extra Sheet.

US CL : 536/23.5; 435/ 69.1, 69.5, 252.3, 320.1; 530/350, 351

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.5; 435/ 69.1, 69.5, 252.3, 320.1; 530/350, 351

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X --- Y	STANGER et al. RIP: A Novel Protein Containing a Death Domain That Interacts with Fas/APO-1 (CD95) in Yeast and Causes Cell Death. Cell. 19 May 1995, Vol. 81, pages 513-523, see Figs. 2-3, and sequence alignment,	1-3 ----- 2
Y, P	WO 96/25941 A1 (YEDA RESEARCH & DEVELOPMENT CO. LTD.) 29 August 1996 (29/08/96), see abstract, figures and claims.	1-3
A	HSU et al. The TNF Receptor 1-Associated Protein TRADD Signals Cell Death and NF-kB Activation. Cell, 19 May 1995, Vol. 81, pages 495-504, see all.	1-3

☒ Further documents are listed in the continuation of Box C.
 ☐ See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*G* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

15 JANUARY 1997

Date of mailing of the international search report

28 FEB 1997

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

GARNETTE D. DRAPER

Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/16778

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A, P	BAKER et al. Transducers of Life and Death: TNF Receptor Superfamily and Associated Proteins. Oncogene, 04 January 1996, Vol. 12, pages 1-9, see all	1-3

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/16778

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-3

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US96/16778

A. CLASSIFICATION OF SUBJECT MATTER:

IPC (6):

C07H 21/04; C12P 21/06, 21/02; C12N 1/20, 15/00; C07K 1/00, 14/52

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claims 1-3, drawn to nucleic acids that encode for human Receptor Interacting Proteins (hRIP) and methods of making the encoded proteins.

Group II, claims 4-7, drawn to methods of identifying lead compounds.

The inventions listed as Groups do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: The special technical feature of Group I is directed to nucleic acids that encode for hRIP and to methods of making hRIP; whereas the special technical feature of Group II is directed to methods of identifying lead compounds. The methods of these two groups do not share a special technical and unifying feature, because each of these methods require the utilization of different process/method steps, different elements/agents, and their are different starting material and the final outcomes are also different. Furthermore, these methods and their steps and elements are not required one for the other.